## AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method of diagnosing schizophrenia comprising:

a) providing a nucleic acid from a human subject suspected of having schizophrenia; wherein said nucleic acid comprises an α7 allele;

b) detecting at least one polymorphism within a core promoter region of said α7 allele, wherein said core promoter region corresponds to SEQ ID NO:125 and wherein said polymorphism comprises a single variant selected from the group consisting of -86C/T; -92G/A, -143 G/A. –178 -G; -180 G/C; -191 G/A; -194 G/C; and -241 A/G, or a dual variant selected from the group consisting of -46/-178; -146/-190; -46/-191; -86/-241; and -178/-191 of SEQ ID NO:125 in relation to a start codon of said α7 allele beginning at residue 270;;

c) interviewing said subject by a physician, wherein said subject presents at least one symptom of schizophrenia; and

d) providing a diagnosis of schizophrenia to said subject based on the presence of said at least one polymorphism and said at least one symptom, wherein said diagnosis differentiates schizophrenia from other forms of mental illness.

2-4. (Canceled)

5. (Original) The method of Claim 1, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

6. (Original) The method of Claim 1, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

7-25. (Canceled)

26. (Currently Amended) A method of identifying individuals predisposed to schizophrenia comprising:

a) providing a nucleic acid from a human subject; wherein said nucleic acid comprises an α7 allele; and

b) detecting at least one polymorphism within SEQ ID NO:125 of said α7 allele, wherein said polymorphism comprises a single variant selected from the group consisting of -86C/T; -92G/A, -143 G/A. –178 -G; -180 G/C; -191 G/A; -194 G/C; and -241 A/G, or a dual variant selected from the group consisting of -46/-178; -146/-190; -46/-191; -86/-241; and -178/-191 of SEQ ID NO:125 in relation to a start codon of said α7 allele beginning at residue 270;

and

c) identifying that said subject is predisposed to schizophrenia by said detected polymorphism.

27-34. (Canceled)

35. (Previously Presented) The method of Claim 26, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

36. (Previously Presented) The method of Claim 26, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

37-41. (Canceled)

42. (Previously Presented) The method of Claim 26, wherein the method further comprises, before step (c) determining a P50 test conditioning ratio.

43. (Previously Presented) The method of Claim 42, wherein the method further comprises step (d) establishing that said subject is predisposed to schizophrenia by said detected polymorphism and said p50 test conditioning ratio of at least 0.5.

44. (Previously Presented) The method of Claim 26, wherein said P50 test conditioning ratio is determined by an auditory hearing response test.

45-46. (Canceled)